

#3 0590  
06/25<sup>OIPE</sup>

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/767,215

DATE: 07/02/2001

TIME: 16:52:23

Input Set : A:\07334-142001.txt

Output Set: N:\CRF3\07022001\I767215.raw

ENTERED

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4 <110> APPLICANT: Bertin, John
6 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
7   PROTEIN FAMILY AND USES THEREOF
9 <130> FILE REFERENCE: 07334-142001
11 <140> CURRENT APPLICATION NUMBER: 09/767,215
12 <141> CURRENT FILING DATE: 2001-01-22
14 <150> PRIOR APPLICATION NUMBER: 60/181,159
15 <151> PRIOR FILING DATE: 2000-02-09
17 <160> NUMBER OF SEQ ID NOS: 10
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 3931
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (207)...(3218)
30 <400> SEQUENCE: 1
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32 gtcccaccca gcagcccga gagaaaggag gcagctggca ccacactggg ctttgagac      120
33 actgcgggga ctgtggaccc caccctgctg caccgagctc ctgcaaaagc aaacctgaga      180
34 accttgggtc ctcccagcgc ccagcc atg ggg gaa ctg tgc cgc agg gac tcc      233
35                               Met Gly Glu Leu Cys Arg Arg Asp Ser
36                               1                               5
38 gca ctc acg gca ctg gac gag gag aca ctg tgg gag atg atg gag agc      281
39 Ala Leu Thr Ala Leu Asp Glu Glu Thr Leu Trp Glu Met Met Glu Ser
40 10                               15                               20                               25
42 cac cgc cac agg atc gta cgc tgc atc tgc ccc agc cgc ctc acc ccc      329
43 His Arg His Arg Ile Val Arg Cys Ile Cys Pro Ser Arg Leu Thr Pro
44                               30                               35                               40
46 tac ctg cgc cag gcc aag gtg ctg tgc cag ctg gac gag gag gag gtg      377
47 Tyr Leu Arg Gln Ala Lys Val Leu Cys Gln Leu Asp Glu Glu Glu Val
48                               45                               50                               55
50 ctg cac agc ccc cgg ctc acc aac agc gcc atg cgg gcc ggg cac ttg      425
51 Leu His Ser Pro Arg Leu Thr Asn Ser Ala Met Arg Ala Gly His Leu
52 60                               65                               70
54 ctg gat ttg ctg aag act cga ggg aag aac ggg gcc atc gcc ttc ctg      473
55 Leu Asp Leu Leu Lys Thr Arg Gly Lys Asn Gly Ala Ile Ala Phe Leu
56 75                               80                               85
58 gag agc ctg aag ttc cac aac cct gac gtc tac acc ctg gtc acc ggg      521
59 Glu Ser Leu Lys Phe His Asn Pro Asp Val Tyr Thr Leu Val Thr Gly
60 90                               95                               100                               105
62 ctg cag cct gat gtt gac ttc agt aac ttt agc ggt ctc atg gag aca      569
63 Leu Gln Pro Asp Val Asp Phe Ser Asn Phe Ser Gly Leu Met Glu Thr
64 110                               115                               120
66 tcc aag ctg acc gag tgc ctg gct ggg gcc atc ggc agc ctg cag gag      617
67 Ser Lys Leu Thr Glu Cys Leu Ala Gly Ala Ile Gly Ser Leu Gln Glu

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68	125	130	135	
70	gag ctg aac cag gaa aag ggg cag aag gag gtg ctg ctg cgg cgg tgc			665
71	Glu Leu Asn Gln Glu Lys Gly Gln Lys Glu Val Leu Leu Arg Arg Cys			
72	140	145	150	
74	cag cag ctg cag gag cac ctg ggc ctg gcc gag acc cgt gcc gag ggc			713
75	Gln Gln Leu Gln Glu His Leu Gly Leu Ala Glu Thr Arg Ala Glu Gly			
76	155	160	165	
78	ctg cac cag ctg gag gct gac cac agc cgc atg aag cgt gag gtt agc			761
79	Leu His Gln Leu Glu Ala Asp His Ser Arg Met Lys Arg Glu Val Ser			
80	170	175	180	185
82	gca cac ttc cat gag gtg ctg agg ctg aag gac gag atg ctc agc ctc			809
83	Ala His Phe His Glu Val Leu Arg Leu Lys Asp Glu Met Leu Ser Leu			
84	190	195	200	
86	tcg ctg cac tat agc aat gcg ctg cag gag aag gag ctg gcc gcc tca			857
87	Ser Leu His Tyr Ser Asn Ala Leu Gln Glu Lys Glu Leu Ala Ala Ser			
88	205	210	215	
90	cgc tgc cgc agc ctg cag gag gag ctg tat cta ctg aag cag gag ctg			905
91	Arg Cys Arg Ser Leu Gln Glu Glu Leu Tyr Leu Leu Lys Gln Glu Leu			
92	220	225	230	
94	cag cga gcc aac atg gtt tcc tcc tgt gag ctg gaa ttg caa gag cag			953
95	Gln Arg Ala Asn Met Val Ser Ser Cys Glu Leu Glu Leu Gln Glu Gln			
96	235	240	245	
98	tcc ctg agg aca gcc agc gac cag gag tcc ggg gat gag gag ctg aac			1001
99	Ser Leu Arg Thr Ala Ser Asp Gln Glu Ser Gly Asp Glu Glu Leu Asn			
100	250	255	260	265
102	cgc ctg aag gag gag aat gag aaa ctg cgc tcg ctg act ttc agc ctg			1049
103	Arg Leu Lys Glu Glu Asn Glu Lys Leu Arg Ser Leu Thr Phe Ser Leu			
104	270	275	280	
106	gcg gag aag gac att ctg gag cag agc ctg gac gag gcg cgg ggg agc			1097
107	Ala Glu Lys Asp Ile Leu Glu Gln Ser Leu Asp Glu Ala Arg Gly Ser			
108	285	290	295	
110	cga cag gag ctg gtg gag cgc atc cac tcg ctg cgg gag cgg gcc gtg			1145
111	Arg Gln Glu Leu Val Glu Arg Ile His Ser Leu Arg Glu Arg Ala Val			
112	300	305	310	
114	gct gcc gag agg cag cga gag cag tac tgg gaa gag aag gaa cag acc			1193
115	Ala Ala Glu Arg Gln Arg Glu Gln Tyr Trp Glu Glu Lys Glu Gln Thr			
116	315	320	325	
118	ctg ctg cag ttc cag aag agt aag atg gcc tgc caa ctc tac agg gag			1241
119	Leu Leu Gln Phe Gln Lys Ser Lys Met Ala Cys Gln Leu Tyr Arg Glu			
120	330	335	340	345
122	aag gtg aat gcg ctg cag gcc cag gtg tgc gag ctg cag aag gag cga			1289
123	Lys Val Asn Ala Leu Gln Ala Gln Val Cys Glu Leu Gln Lys Glu Arg			
124	350	355	360	
126	gac cag gcg tac tcc gcg agg gac agt gct cag agg gag att tcc cag			1337
127	Asp Gln Ala Tyr Ser Ala Arg Asp Ser Ala Gln Arg Glu Ile Ser Gln			
128	365	370	375	
130	agc ctg gtg gag aag gac tcc ctc cgc agg cag gtg ttc gag ctg acg			1385
131	Ser Leu Val Glu Lys Asp Ser Leu Arg Arg Gln Val Phe Glu Leu Thr			
132	380	385	390	

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134	gac	cag	gtc	tgc	gag	ctg	cgc	aca	cag	ctt	cgc	cag	ctg	cag	gca	gag	1433
135	Asp	Gln	Val	Cys	Glu	Leu	Arg	Thr	Gln	Leu	Arg	Gln	Leu	Gln	Ala	Glu	
136		395					400					405					
138	cct	ccg	ggt	gtg	ctc	aag	cag	gaa	gcc	agg	acc	agg	gag	ccc	tgt	cca	1481
139	Pro	Pro	Gly	Val	Leu	Lys	Gln	Glu	Ala	Arg	Thr	Arg	Glu	Pro	Cys	Pro	
140	410					415					420					425	
142	cgg	gag	aag	cag	cgg	ctg	gtg	cgg	atg	cat	gcc	atc	tgc	ccc	aga	gac	1529
143	Arg	Glu	Lys	Gln	Arg	Leu	Val	Arg	Met	His	Ala	Ile	Cys	Pro	Arg	Asp	
144				430						435					440		
146	gac	agc	gac	tgc	agc	ctc	gtc	agc	tcc	aca	gag	tct	cag	ctc	ttg	tcg	1577
147	Asp	Ser	Asp	Cys	Ser	Leu	Val	Ser	Ser	Thr	Glu	Ser	Gln	Leu	Leu	Ser	
148				445						450					455		
150	gac	ctg	agt	gcc	acg	tcc	agc	cgc	gag	ctg	gtg	gac	agc	ttc	cgc	tcc	1625
151	Asp	Leu	Ser	Ala	Thr	Ser	Ser	Arg	Glu	Leu	Val	Asp	Ser	Phe	Arg	Ser	
152			460					465					470				
154	agc	agc	ccc	gcg	ccc	ccc	agc	cag	cag	tcc	ctg	tac	aag	cgg	gtg	gcc	1673
155	Ser	Ser	Pro	Ala	Pro	Pro	Ser	Gln	Gln	Ser	Leu	Tyr	Lys	Arg	Val	Ala	
156		475					480						485				
158	gag	gac	ttc	ggg	gaa	gaa	ccc	tgg	tct	ttc	agc	agc	tgc	ctg	gag	atc	1721
159	Glu	Asp	Phe	Gly	Glu	Glu	Pro	Trp	Ser	Phe	Ser	Ser	Cys	Leu	Glu	Ile	
160	490					495					500					505	
162	ccg	gag	gga	gac	ccg	gga	gcc	ctg	ccg	gga	gct	aag	gca	ggc	gac	cca	1769
163	Pro	Glu	Gly	Asp	Pro	Gly	Ala	Leu	Pro	Gly	Ala	Lys	Ala	Gly	Asp	Pro	
164				510						515					520		
166	cac	ctg	gat	tat	gag	ctc	cta	gac	acg	gca	gac	ctt	ccg	cag	ctg	gaa	1817
167	His	Leu	Asp	Tyr	Glu	Leu	Leu	Asp	Thr	Ala	Asp	Leu	Pro	Gln	Leu	Glu	
168				525						530					535		
170	agc	agc	ctg	cag	cca	gtc	tcc	cct	gga	agg	ctt	gat	gtc	tcg	gag	agc	1865
171	Ser	Ser	Leu	Gln	Pro	Val	Ser	Pro	Gly	Arg	Leu	Asp	Val	Ser	Glu	Ser	
172			540					545					550				
174	ggc	gtc	ctc	atg	cgg	cgg	agg	cca	gcc	cgc	agg	atc	ctg	agc	cag	gtc	1913
175	Gly	Val	Leu	Met	Arg	Arg	Arg	Pro	Ala	Arg	Arg	Ile	Leu	Ser	Gln	Val	
176		555					560					565					
178	acc	atg	ctg	gcg	ttc	cag	ggg	gat	gca	ttg	ctg	gag	cag	atc	agc	gtc	1961
179	Thr	Met	Leu	Ala	Phe	Gln	Gly	Asp	Ala	Leu	Leu	Glu	Gln	Ile	Ser	Val	
180	570					575					580					585	
182	atc	ggc	ggg	aac	ctc	acg	ggc	atc	ttc	atc	cac	cgg	gtc	acc	ccg	ggc	2009
183	Ile	Gly	Gly	Asn	Leu	Thr	Gly	Ile	Phe	Ile	His	Arg	Val	Thr	Pro	Gly	
184				590						595					600		
186	tcg	gcg	gcg	gac	cag	atg	gcc	ttg	cgc	ccg	ggc	acc	cag	att	gtg	atg	2057
187	Ser	Ala	Ala	Asp	Gln	Met	Ala	Leu	Arg	Pro	Gly	Thr	Gln	Ile	Val	Met	
188			605							610					615		
190	gtt	gat	tac	gaa	gcc	tca	gag	ccc	ttg	ttc	aag	gca	gtc	ctg	gag	gac	2105
191	Val	Asp	Tyr	Glu	Ala	Ser	Glu	Pro	Leu	Phe	Lys	Ala	Val	Leu	Glu	Asp	
192			620							625					630		
194	acg	acc	ctg	gag	gag	gcc	gtg	ggg	ctt	ctc	agg	agg	gtg	gac	ggc	ttc	2153
195	Thr	Thr	Leu	Glu	Glu	Ala	Val	Gly	Leu	Leu	Arg	Arg	Val	Asp	Gly	Phe	
196		635					640					645					
198	tgc	tgc	ctg	tct	gtg	aag	gtc	aac	acg	gac	ggt	tat	aag	agg	cta	ctc	2201

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199	Cys	Cys	Leu	Ser	Val	Lys	Val	Asn	Thr	Asp	Gly	Tyr	Lys	Arg	Leu	Leu	
200	650					655					660					665	
202	cag	gac	ctg	gag	gcc	aaa	gtg	gcg	acc	tcg	ggg	gac	tca	ttc	tac	atc	2249
203	Gln	Asp	Leu	Glu	Ala	Lys	Val	Ala	Thr	Ser	Gly	Asp	Ser	Phe	Tyr	Ile	
204					670					675					680		
206	cgg	gtc	aac	ctg	gcc	atg	gag	ggc	agg	gcc	aaa	ggg	gag	ctg	cag	gtg	2297
207	Arg	Val	Asn	Leu	Ala	Met	Glu	Gly	Arg	Ala	Lys	Gly	Glu	Leu	Gln	Val	
208					685					690					695		
210	cat	tgc	aac	gag	gtc	ctg	cac	gtc	acc	gac	acc	atg	ttc	cag	ggc	tgc	2345
211	His	Cys	Asn	Glu	Val	Leu	His	Val	Thr	Asp	Thr	Met	Phe	Gln	Gly	Cys	
212			700						705				710				
214	ggc	tgc	tgg	cat	gcc	cac	cgc	gtg	aac	tct	tac	acc	atg	aag	gat	act	2393
215	Gly	Cys	Trp	His	Ala	His	Arg	Val	Asn	Ser	Tyr	Thr	Met	Lys	Asp	Thr	
216		715					720					725					
218	gcc	gcg	cac	ggc	acc	atc	ccc	aac	tac	tcc	agg	gct	cag	cag	cag	ctc	2441
219	Ala	Ala	His	Gly	Thr	Ile	Pro	Asn	Tyr	Ser	Arg	Ala	Gln	Gln	Gln	Leu	
220	730					735					740					745	
222	ata	gcc	ctc	atc	cag	gac	atg	act	cag	cag	tgc	acc	gtg	acc	cgc	aag	2489
223	Ile	Ala	Leu	Ile	Gln	Asp	Met	Thr	Gln	Gln	Cys	Thr	Val	Thr	Arg	Lys	
224					750					755					760		
226	cca	tct	tct	ggg	gga	cca	cag	aag	ctg	gtc	cgc	atc	gtc	agt	atg	gac	2537
227	Pro	Ser	Ser	Gly	Gly	Pro	Gln	Lys	Leu	Val	Arg	Ile	Val	Ser	Met	Asp	
228					765					770					775		
230	aaa	gcc	aag	gcc	agc	cct	ctg	cgt	ttg	tcc	ttt	gac	agg	ggc	cag	ttg	2585
231	Lys	Ala	Lys	Ala	Ser	Pro	Leu	Arg	Leu	Ser	Phe	Asp	Arg	Gly	Gln	Leu	
232			780							785				790			
234	gac	ccc	agc	agg	atg	gag	ggc	tcc	agc	acg	tgc	ttc	tgg	gcc	gag	agc	2633
235	Asp	Pro	Ser	Arg	Met	Glu	Gly	Ser	Ser	Thr	Cys	Phe	Trp	Ala	Glu	Ser	
236			795				800					805					
238	tgc	ctc	acc	ctg	gtg	ccc	tat	acc	ctg	gtg	tgg	ccc	cat	cga	ccc	gcc	2681
239	Cys	Leu	Thr	Leu	Val	Pro	Tyr	Thr	Leu	Val	Trp	Pro	His	Arg	Pro	Ala	
240	810					815					820					825	
242	cgg	ccc	cgg	cct	gtg	ctc	ctc	gtg	ccc	agg	gcg	gtt	ggg	aag	atc	ctg	2729
243	Arg	Pro	Arg	Pro	Val	Leu	Leu	Val	Pro	Arg	Ala	Val	Gly	Lys	Ile	Leu	
244					830					835					840		
246	agc	gag	aaa	ctg	tgc	ctc	ctc	caa	ggg	ttt	aag	aag	tgc	ctg	gca	gag	2777
247	Ser	Glu	Lys	Leu	Cys	Leu	Leu	Gln	Gly	Phe	Lys	Lys	Cys	Leu	Ala	Glu	
248					845					850					855		
250	tac	ttg	agc	cag	gag	gag	tat	gag	gcc	tgg	agc	cag	aga	ggg	gac	atc	2825
251	Tyr	Leu	Ser	Gln	Glu	Glu	Tyr	Glu	Ala	Trp	Ser	Gln	Arg	Gly	Asp	Ile	
252			860							865				870			
254	atc	cag	gag	gga	gag	gtg	tcc	ggg	ggc	cgc	tgc	tgg	gtg	acc	cgc	cat	2873
255	Ile	Gln	Glu	Gly	Glu	Val	Ser	Gly	Gly	Arg	Cys	Trp	Val	Thr	Arg	His	
256			875				880					885					
258	gct	gtg	gag	tcc	ctc	atg	gaa	aag	aac	acc	cat	gcc	ctc	ctg	gac	gtc	2921
259	Ala	Val	Glu	Ser	Leu	Met	Glu	Lys	Asn	Thr	His	Ala	Leu	Leu	Asp	Val	
260	890					895					900					905	
262	cag	ctg	gac	agt	gtc	tgc	acc	ctg	cac	agg	atg	gac	atc	ttc	ccc	atc	2969
263	Gln	Leu	Asp	Ser	Val	Cys	Thr	Leu	His	Arg	Met	Asp	Ile	Phe	Pro	Ile	

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264          910          915          920
266 gtc atc cac gtc tct gtc aac gag aag atg gca aag aag ctc aag aag      3017
267 Val Ile His Val Ser Val Asn Glu Lys Met Ala Lys Lys Leu Lys Lys
268          925          930          935
270 ggc cta cag cgg ttg ggc acc tca gag gag cag ctc ctg gag gct gcg      3065
271 Gly Leu Gln Arg Leu Gly Thr Ser Glu Glu Gln Leu Leu Glu Ala Ala
272          940          945          950
274 agg cag gag gag gga gac ctg gac cgg gcg ccc tgt cta tac agc agc      3113
275 Arg Gln Glu Glu Gly Asp Leu Asp Arg Ala Pro Cys Leu Tyr Ser Ser
276          955          960          965
278 ctg gct cct gac ggc tgg agc gac ctg gac ggc ctg ctc agc tgt gtc      3161
279 Leu Ala Pro Asp Gly Trp Ser Asp Leu Asp Gly Leu Leu Ser Cys Val
280 970          975          980          985
282 cgc cag gcc atc gcc gac gag cag aag aag gtg gtg tgg acg gag cag      3209
283 Arg Gln Ala Ile Ala Asp Glu Gln Lys Lys Val Val Trp Thr Glu Gln
284          990          995          1000
286 agc ccc cga tga tgcaccg tgcccccttc cgggactgtg ggggcttctg      3258
287 Ser Pro Arg
290 tgtgctgtt aatgcagtc ttgtctcag cccaggccct cttggcacag ctgtgggctc      3318
291 cttggcacat gaggccggt ctccccactg gctggggtct aaccttgaac cctcaccacg      3378
292 tgcaggtcac acacagtga gccacttgta actgcacact tttctgtgga aacatcttca      3438
293 cccctttacca ggcttggcat ggtctgaact ggaaaccctg agaatgtttc tgcagtagga      3498
294 caggagggac atcttcccat gccttcccta gaaccggagg ccccgactt ctctggaaaa      3558
295 ccgcctgtct gcaggcccg tcaaatcta tgggggctgc acttccctt tacattttga      3618
296 tgtgtcaaag gcttttgag tgacaaaag cacagaggca gcgggtgggg cgcctgggtg      3678
297 gtcccaagg tgcgtgccac ccttgcccgg ggcagaggca taagcccaca tatgctgtga      3738
298 cgctggccac cttttctcag cttctgaggc tgcgatgcct caggaactcc agtttacaga      3798
299 gaccagtgtg tttacttgta aataaagcct ctgggtgggt gagacggtac tttcagtggt      3858
300 tctgtgcccc gtggcccctg tgccgtgtcg gtgggggtgt cccagagaag cctggcacca      3918
301 gtacccccgt caa      3931
303 <210> SEQ ID NO: 2
304 <211> LENGTH: 1004
305 <212> TYPE: PRT
306 <213> ORGANISM: Homo sapiens
308 <400> SEQUENCE: 2
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310 1          5          10          15
311 Glu Thr Leu Trp Glu Met Met Glu Ser His Arg His Arg Ile Val Arg
312          20          25          30
313 Cys Ile Cys Pro Ser Arg Leu Thr Pro Tyr Leu Arg Gln Ala Lys Val
314          35          40          45
315 Leu Cys Gln Leu Asp Glu Glu Glu Val Leu His Ser Pro Arg Leu Thr
316          50          55          60
317 Asn Ser Ala Met Arg Ala Gly His Leu Leu Asp Leu Leu Lys Thr Arg
318 65          70          75          80
319 Gly Lys Asn Gly Ala Ile Ala Phe Leu Glu Ser Leu Lys Phe His Asn
320          85          90          95
321 Pro Asp Val Tyr Thr Leu Val Thr Gly Leu Gln Pro Asp Val Asp Phe
322          100          105          110

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